



Examination of Rapidly Mutating Y-STR Loci for Increased Resolution of Common Haplotypes Using a Large Multiplex Kit

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National Institute of Standards and Technology

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NIST and NIJ Disclaimer

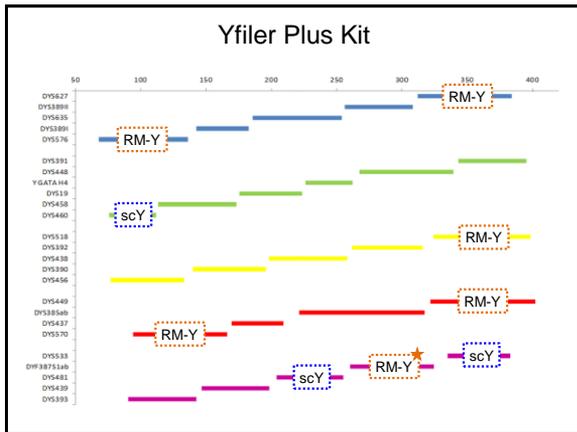
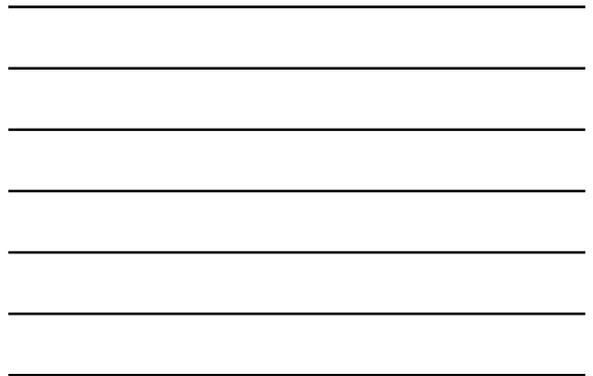
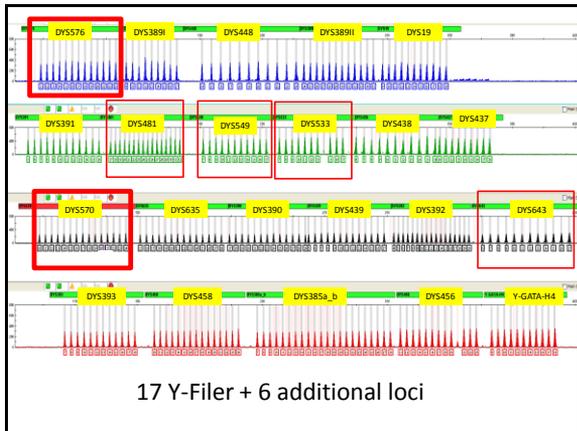
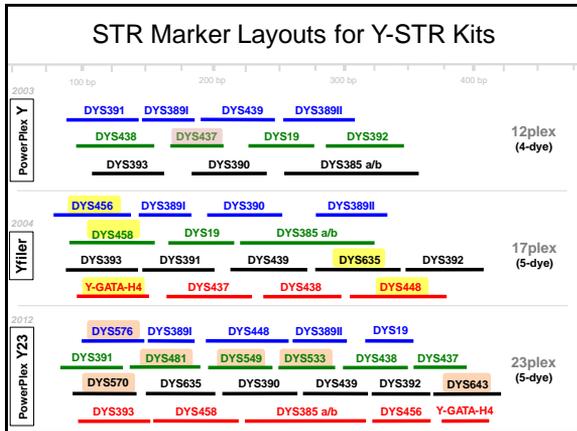
Past and Present Funding: Interagency Agreement between the National Institute of Justice and NIST Office of Law Enforcement Standards

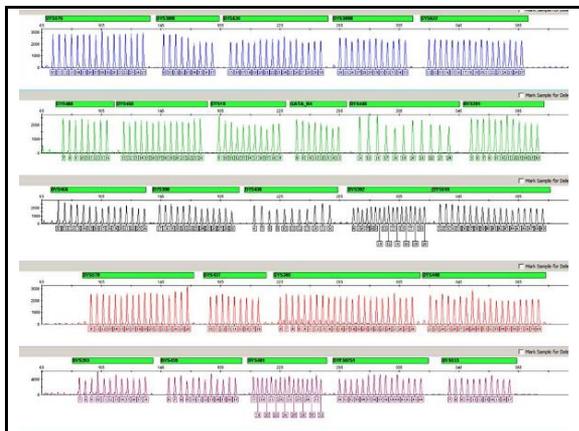
Points of view are mine and do not necessarily represent the official position or policies of the US Department of Justice or the National Institute of Standards and Technology.

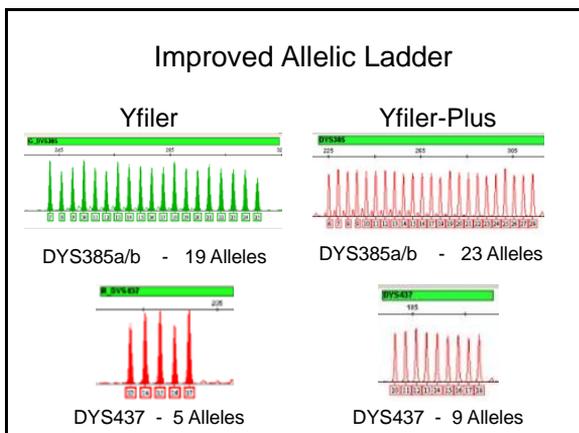
Certain commercial equipment, instruments, software and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

What has happened in the past decade...

- **Selection of core Y-STR loci** (SWGAM Jan 2003)
- "Full" Y-chromosome sequence became available in June 2003; over 700 Y-STR loci identified (only ~20 in 2000)
- **Commercial Y-STR kits released**
 - Y-**P**LEX-6,5,12 (2001-03), **PowerPlex Y** (9/03), **Yfiler** (12/04), **PPY23** (6/12)
 - Yfiler Plus** (since 2014)
- Many population studies performed and online databases generated with thousands of Y-STR haplotypes
- Forensic casework demonstrations showing value of Y-STR testing along with court acceptance
- Renewed interest in Y-STRs to aid familial searching







Disadvantages of the Y-Chromosome

- Loci are not independent of one another and therefore rare random match probabilities cannot be generated with the product rule; must use haplotypes (combination of alleles observed at all tested loci)
- **Not as informative as autosomal STR results**
 - More like addition ($10 + 10 + 10 = 30$) than multiplication ($10 \times 10 \times 10 = 1,000$)
- **Paternal lineages possess the same Y-STR haplotype** (barring mutation) and thus fathers, sons, brothers, uncles, and paternal cousins cannot be distinguished from one another

Rapidly Mutating (RM) Y-STRs

Trying to separate close male relatives



Rapidly Mutating Y-STRs

The American Journal of Human Genetics 87, 341–353, September 10, 2010 ARTICLE

Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications

Kaye N. Ballantyne^{1,2}, Miriam Goedbloed³, Rixun Fang², Onno Schamp⁴, Oscar Lao¹, Andreas Wollstein^{1,3}, Ying Choi¹, Kate van Duijn¹, Mark Vermeulen¹, Silke Brauer^{1,4}, Bonny Decorte³, Micaela Poetsch⁶, Nicole von Wurmb-Schwarz⁷, Peter de Knijff⁸, Damian Labuda⁹, Hlédene Vézina¹⁰, Hans Kookkhanh¹¹, Bülalger Leisig¹², Lutz Roewer¹³, Rafal Florki¹⁴, Tadeusz Dobosz¹⁵, Lotte Henke¹⁶, Jürgen Henke¹⁶, Manohar R. Furtado¹⁷, and Manfred Kayser^{1,4}



Manfred Kayser

Forensic Science International: Genetics 6 (2012) 208–218

Contents lists available at ScienceDirect

Forensic Science International: Genetics

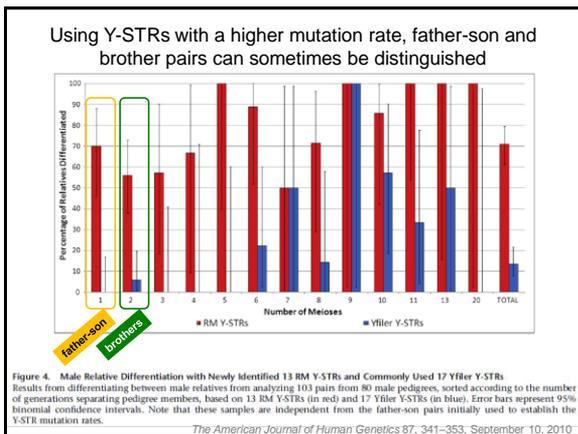
journal homepage: www.elsevier.com/locate/fsig

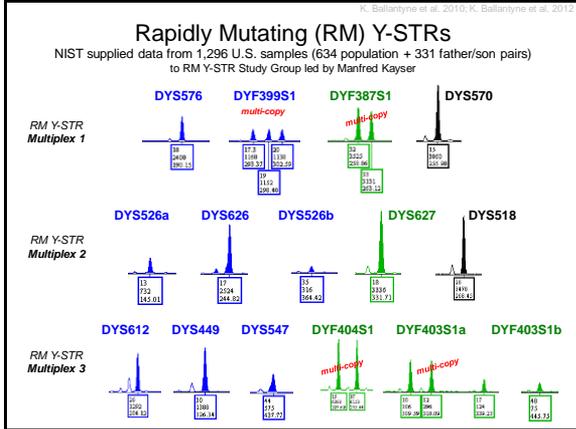
A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages

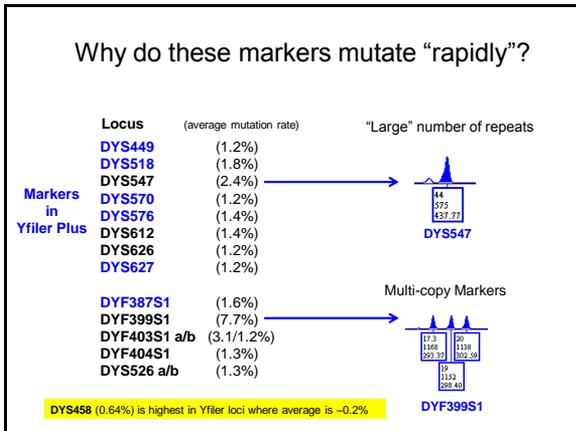
Kaye N. Ballantyne^{1,2}, Victoria Keerl^{4,3}, Andreas Wollstein¹⁶, Ying Choi¹, Soňa B. Zúñiga¹, Arwin Ralf⁴, Mark Vermeulen³, Peter de Knijff⁸, Manfred Kayser¹⁶

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⁴Department of Biostatistics, London University Medical Center, 2009 WC London, The Netherlands

13 markers evaluated







Discrimination Capacity

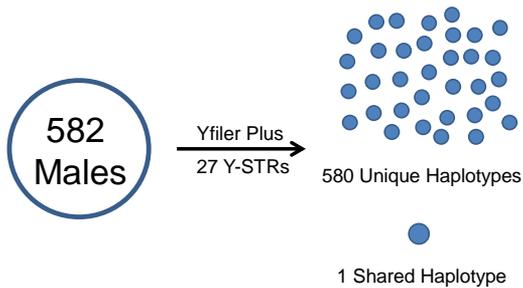
- is a measure of the number of unique haplotypes in a given population

$$DC = \frac{\#H}{N}$$

↖ # of Haplotypes

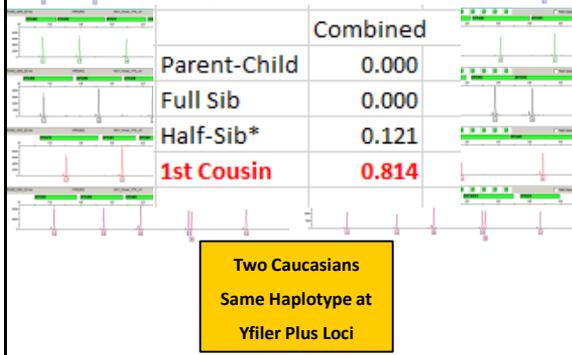
↖ Population size

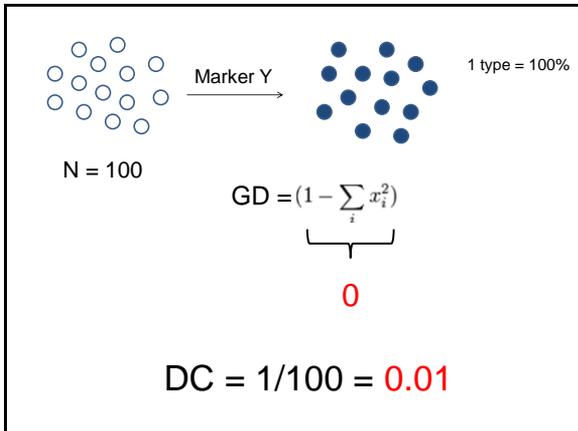
Results so far (582 individuals)

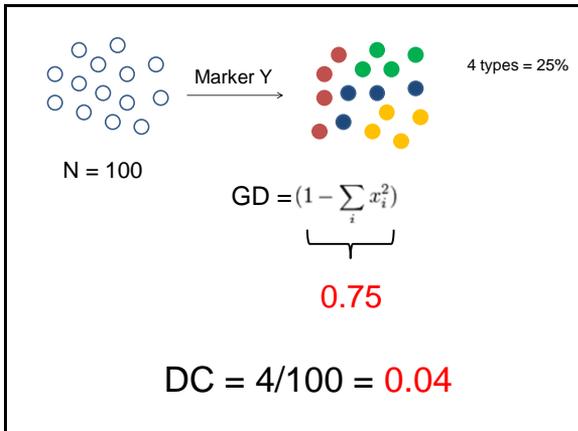


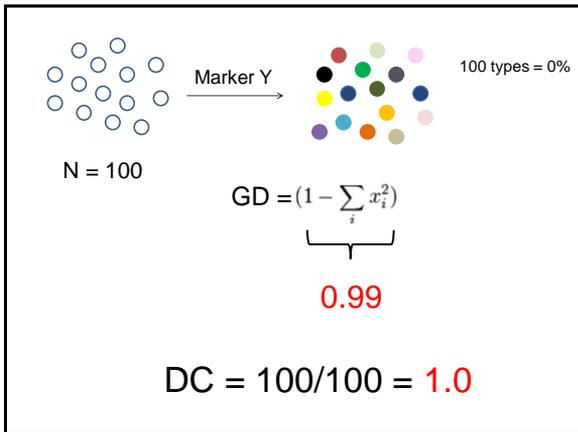
DC = 0.998

Kinship stats over 24 aSTRs



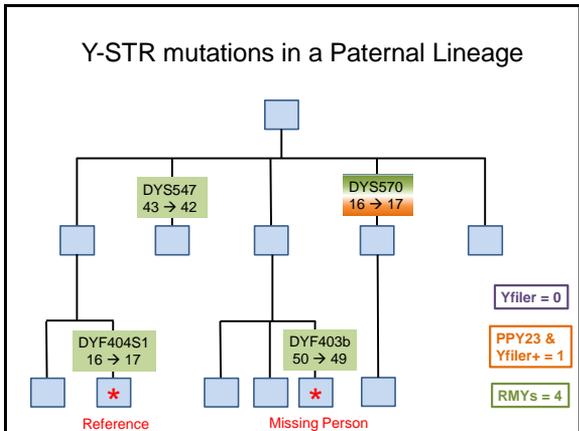






Gene Diversity of the YFP Markers

Locus	Gene Diversity
DYF387S1a/b	0.919
DYS385a/b	0.919
DYS627	0.8584
DYS449	0.8315
DYS481	0.82
DYS518	0.8196
DYS576	0.7954
DYS570	0.7852
DYS458	0.7671
DYS390	0.7645
DYS635	0.7457
DYS389II	0.7375
DYS448	0.7202
DYS456	0.7015
DYS438	0.693
DYS19	0.6681
DYS439	0.6533
DYS533	0.6372
DYS437	0.6305
GATA_H4	0.6026
DYS392	0.6001
DYS460	0.5736
DYS389I	0.548
DYS391	0.5352
DYS393	0.4749



Mutation Rate Information

Meioses	Mutations	Group
63	15	AfAm
89	25	Asian
91	11	Caucasian
88	20	Hispanic
331	71	total (21.4%)

Marker	# of Mutations
DYF399S1	15
DYF403S1a/b	11
DYS627	7
DYS612	7
DYS518	6
DYS570	5
DYS626	5
DYS547	4
DYS526a/b	3
DYS576	3
DYS449	3
DYF404S1	1
DYF387S1	1

+1 Repeat (Son)	-1 Repeat (Son)	Group
8	6	AfAm
11	13	Asian
5	6	Caucasian
8	12	Hispanic

+2 Repeat (Son)	-2 Repeat (Son)	Group
0	1	AfAm
1	0	Asian
0	0	Caucasian
0	0	Hispanic

Interpretational Issues

- We will need to move away from simply “excluding” based upon a number of discordant markers.
- A Likelihood Ratio can provide weight to the evidence based upon competing propositions.
- This will require information on the haplotype frequency and mutation rate data.

Relating two deep-rooted pedigrees from Central Germany by high-resolution Y-STR haplotyping
Manfred Kayser^{a,*}, Mark Vermeulen^{ab}, Hans Knoblauch^c, Herbert Schuster^d,
Michael Krawczak^e, Lutz Roewer^f
Forensic Science International: Genetics 1 (2007) 125–128.

Summary

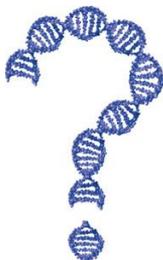
- Rapidly Mutating Y-STRs are highly diverse markers that can discriminate common haplotypes and close relatives.
- These markers may create interpretational issues for paternity/missing persons cases, but LR's can be useful for evaluating these situations.

Acknowledgments

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Arwin Ralf



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